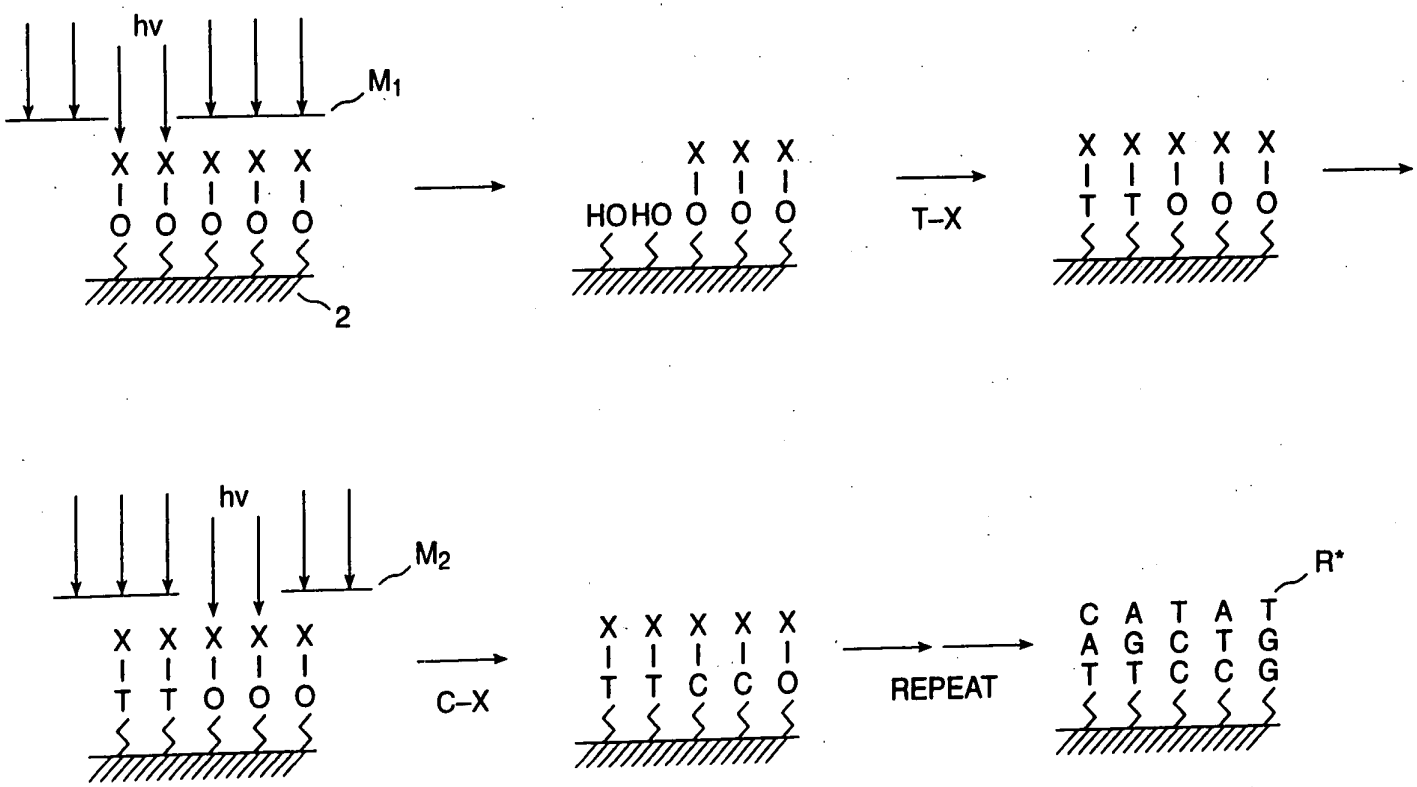

hv
M1
X X X X X
O O O O O
2
HO HO
T-X
T T
C-X
M2
C A T A T
A G T C C
T C C T G
G
R*
REPEAT

FIG. 1

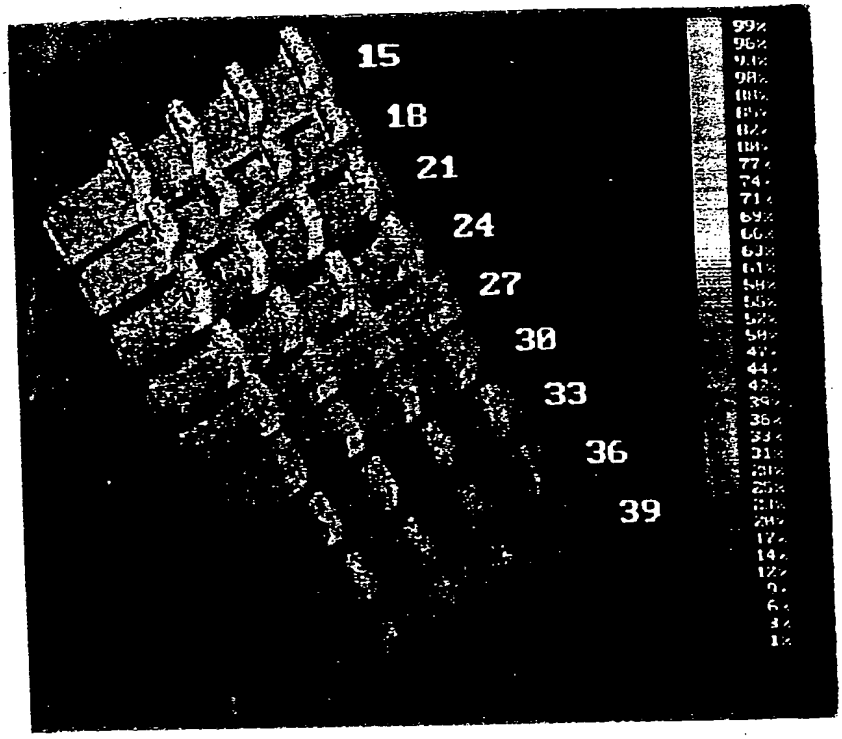


FIG. 2

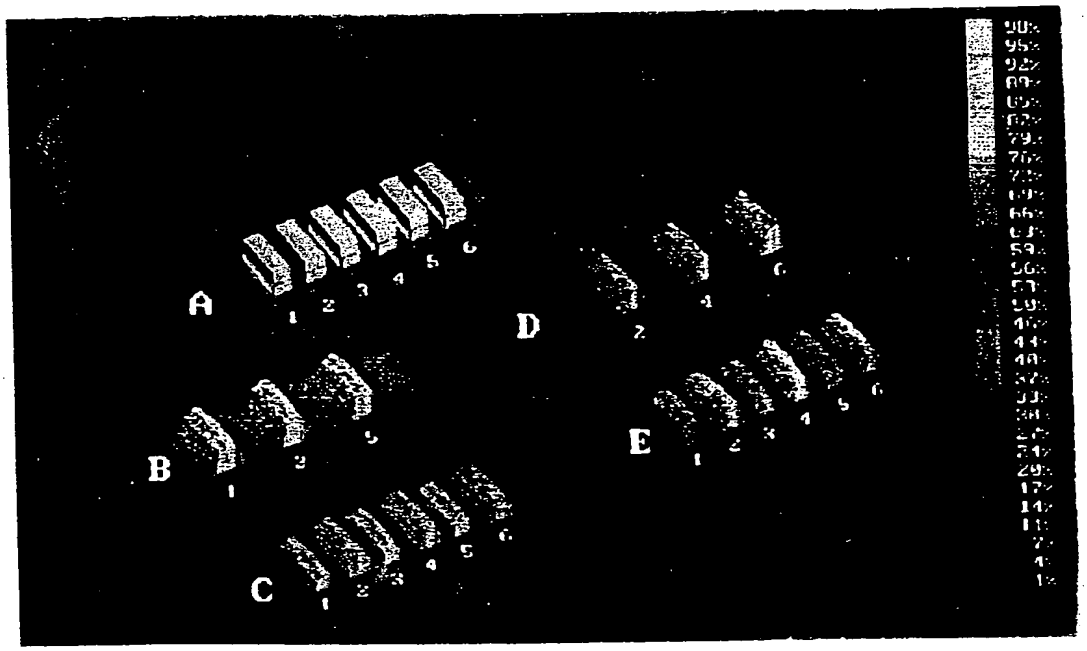


FIG. 3

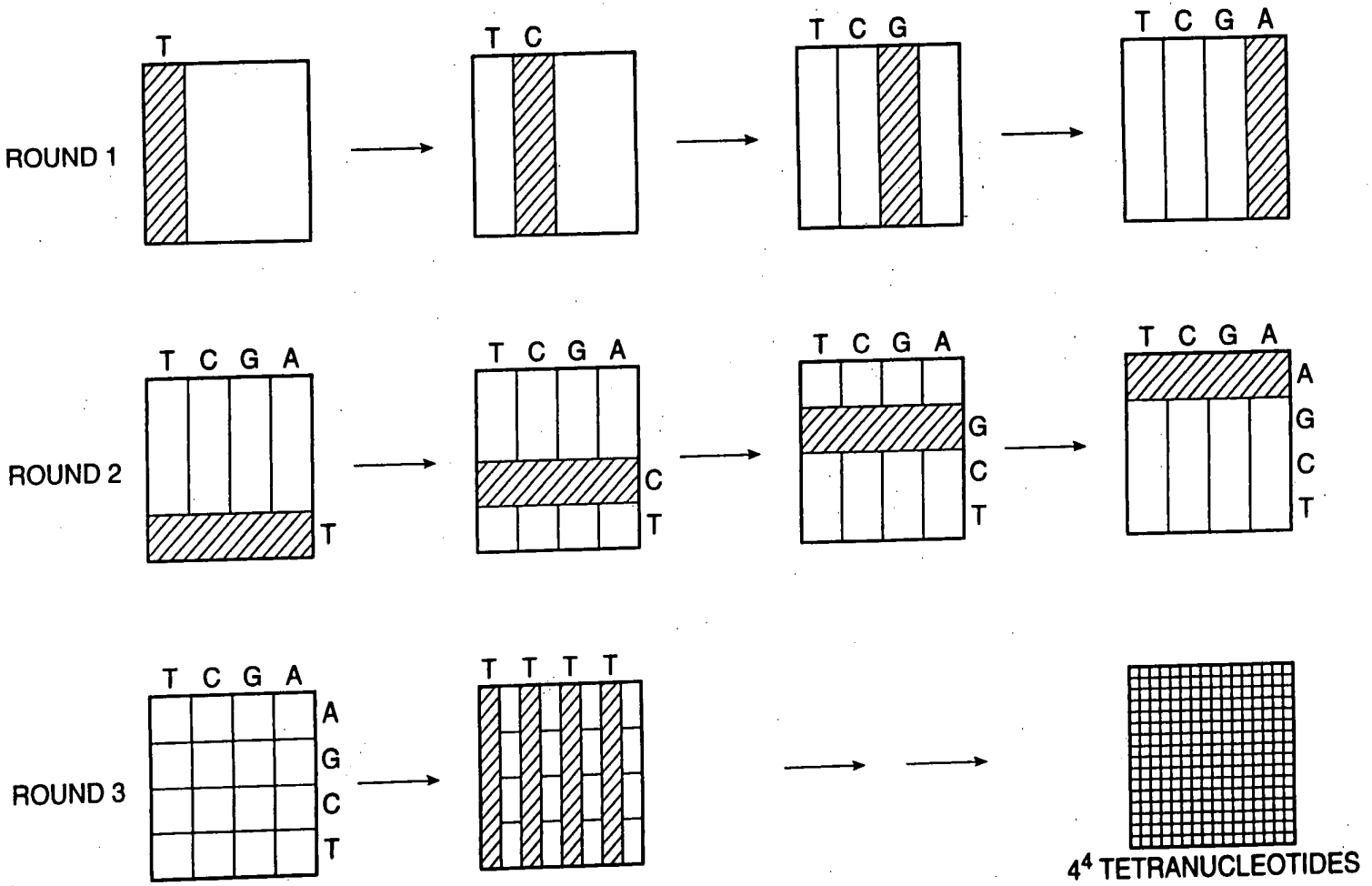

ROUND 1
T
T C
T C G
T C G A
ROUND 2
T C G A
T
T C G A
C
T
T C G A
G
C
T
T C G A
A
G
C
T
ROUND 3
T C G A
A
G
C
T
T T T T
4⁴ TETRANUCLEOTIDES

FIG. 4

FIG. 5a

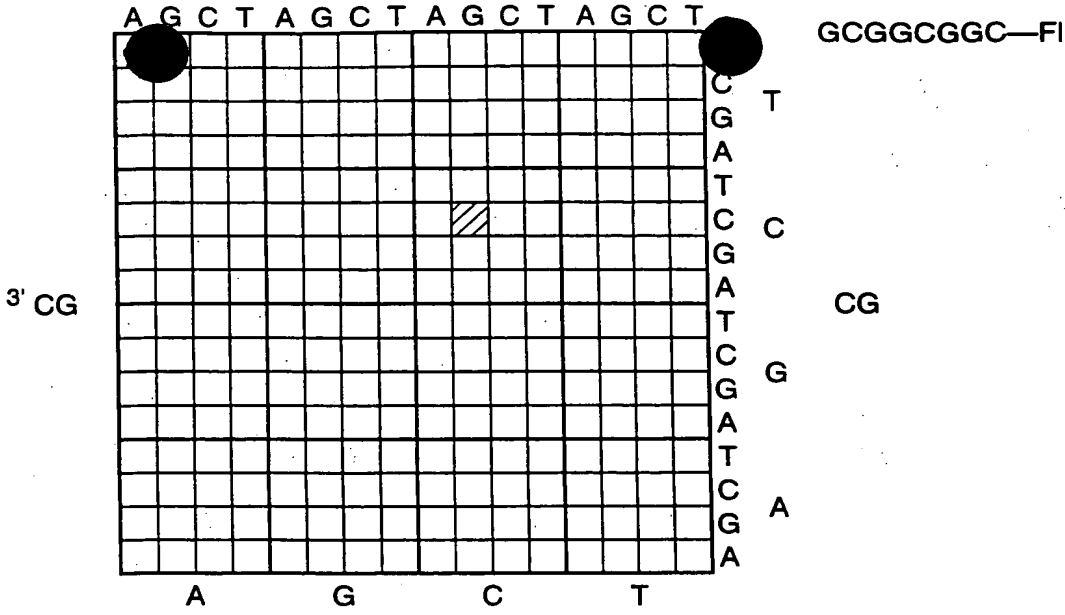


FIG. 5b

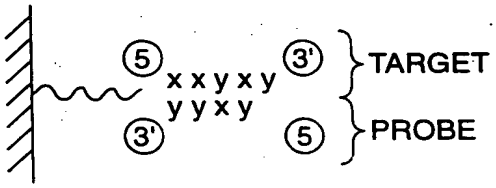


FIG. 6a

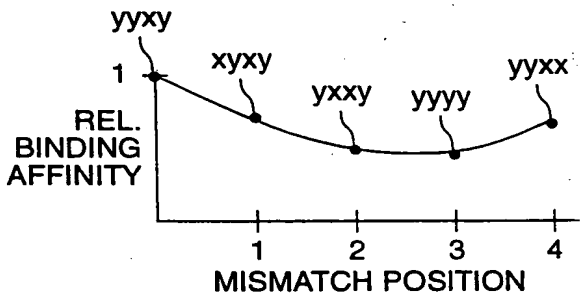


FIG. 6b

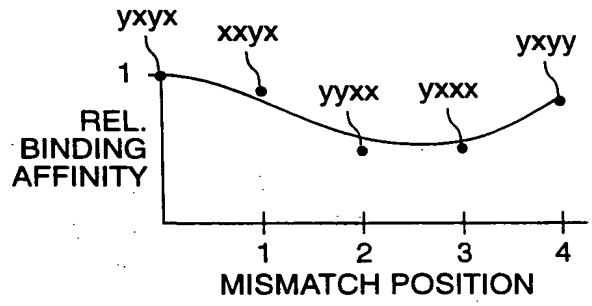


FIG. 6c

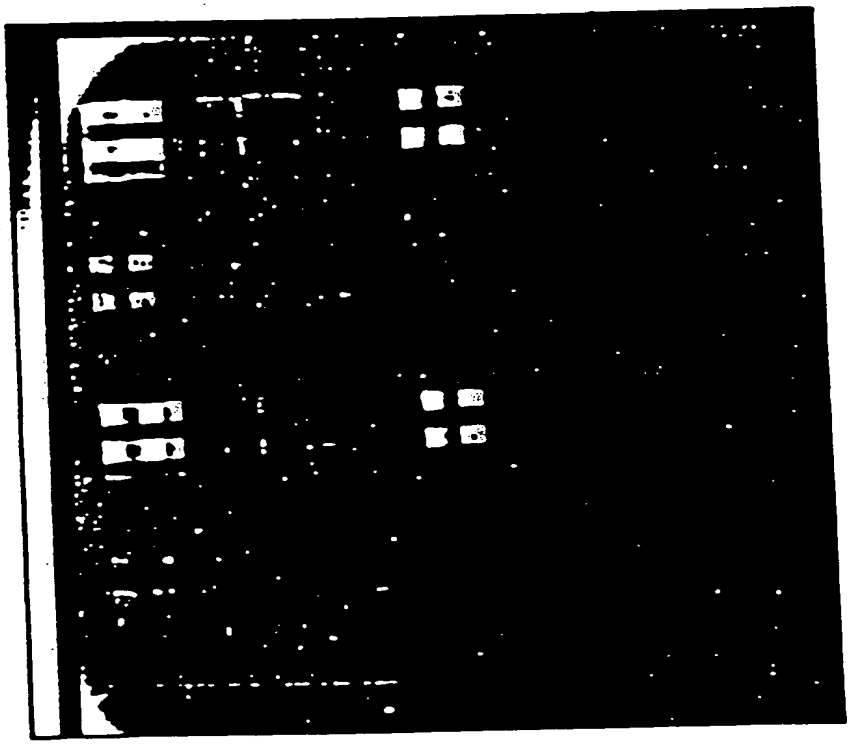


FIG. 7

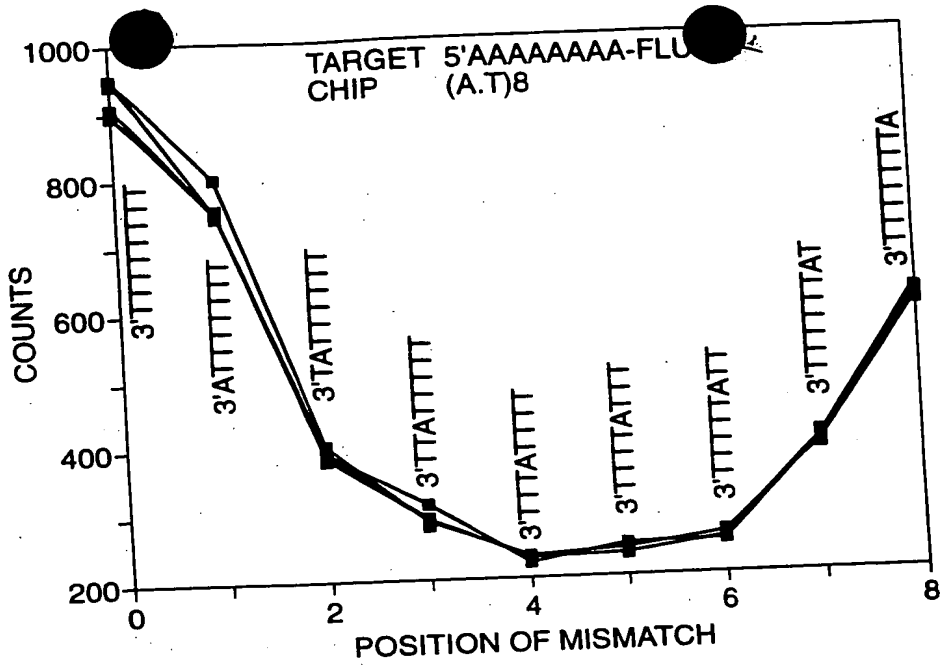

TARGET 5'AAAAAAAA-FLU
CHIP (A.T)8
1000
800
600
400
200
COUNTS
0
2
4
6
8
POSITION OF MISMATCH
3'TTTTTTTT
3'ATTTTTTT
3'TATTTTTT
3'TTATTTTT
3'TTTATTTT
3'TTTTATTT
3'TTTTTAT
3'TTTTTTTA

FIG. 8

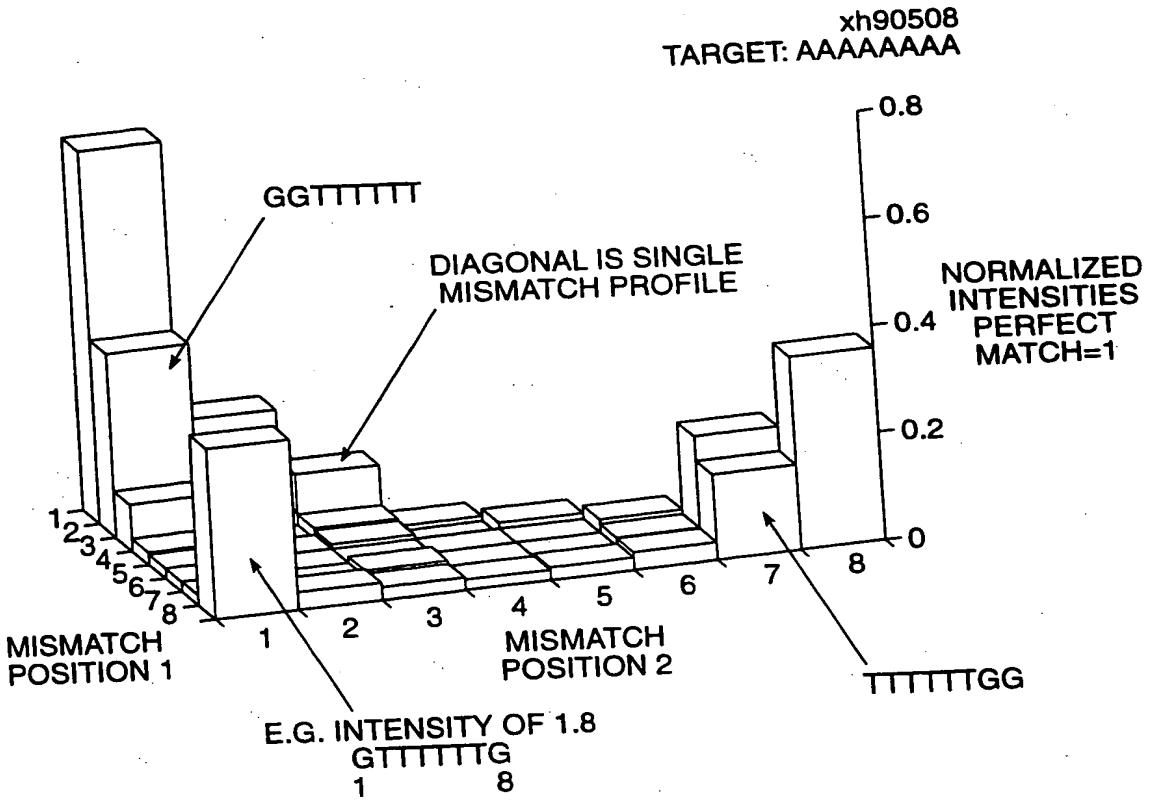

xh90508
TARGET: AAAAAAAA
GGTTTTTT
DIAGONAL IS SINGLE
MISMATCH PROFILE
NORMALIZED
INTENSITIES
PERFECT
MATCH=1
0.8
0.6
0.4
0.2
0
MISMATCH
POSITION 1
MISMATCH
POSITION 2
1
2
3
4
5
6
7
8
TTTTTTGG
E.G. INTENSITY OF 1.8
GTTTTTTG
1
8

FIG. 9

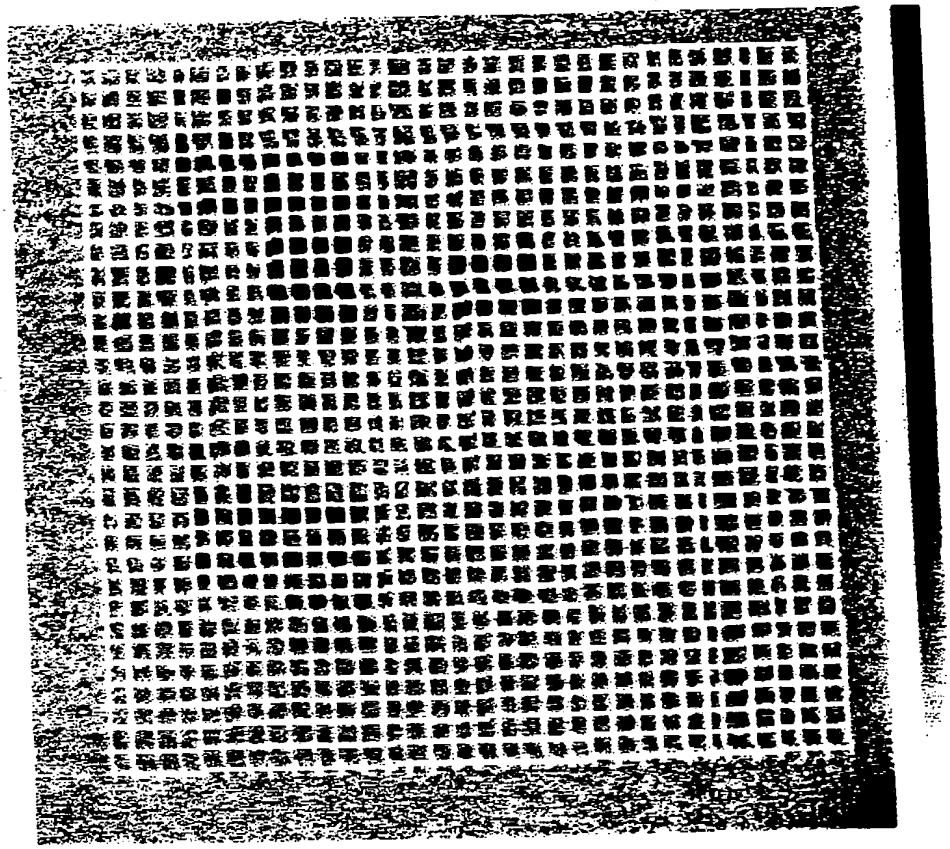
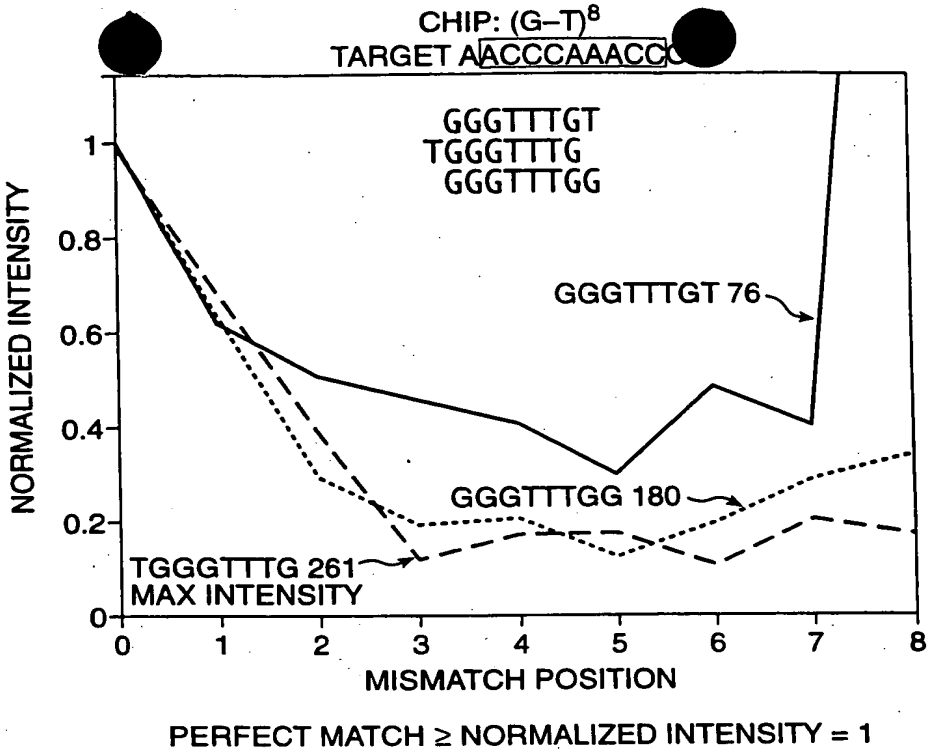


FIG. 10



PERFECT MATCH ≥ NORMALIZED INTENSITY = 1

FIG. 11a

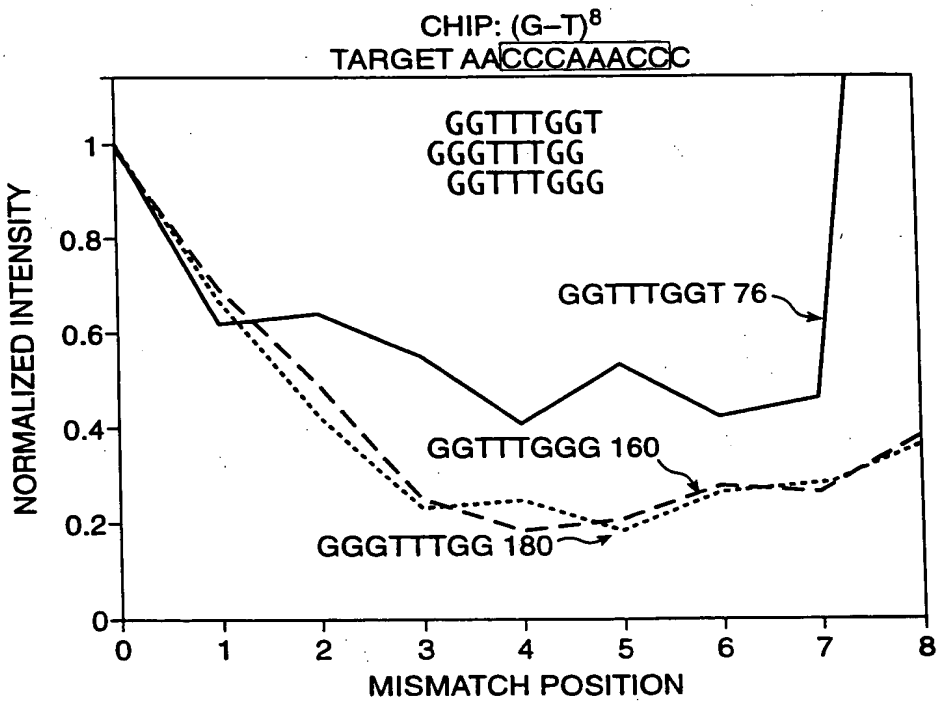


FIG. 11b

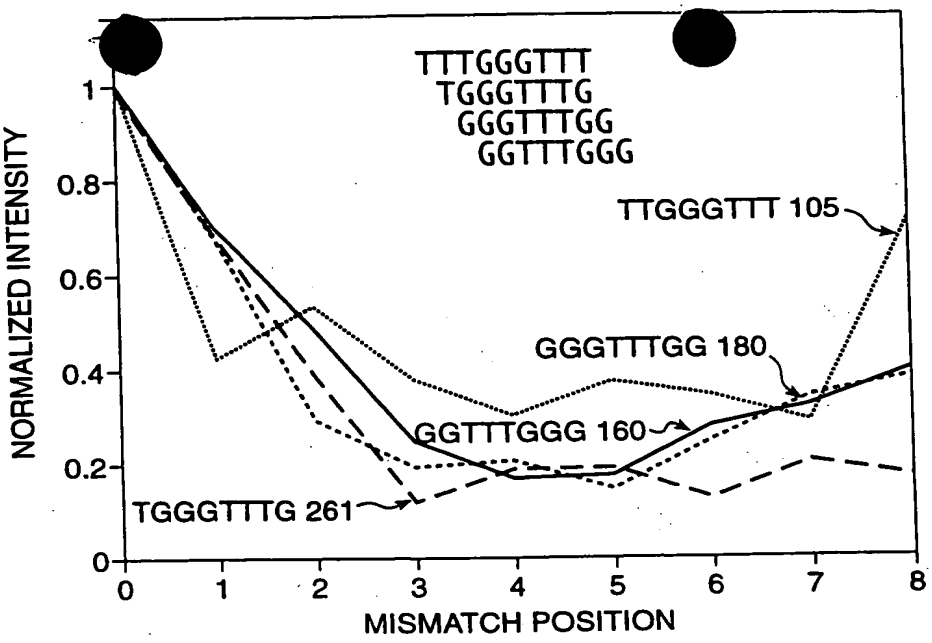


FIG. 11c

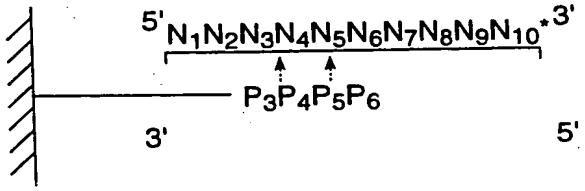


FIG. 12a

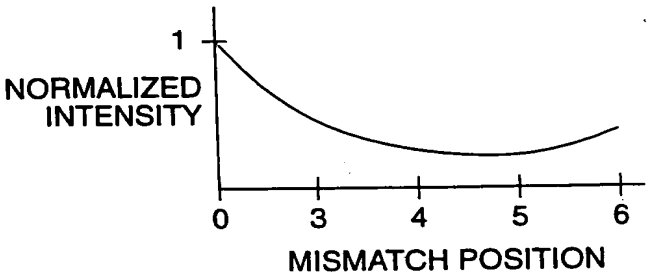


FIG. 12b

A P_3 P_4 P_5
T P_3 P_4 P_5
C P_3 P_4 P_5
T P_3 P_4 P_5

FIG. 12c

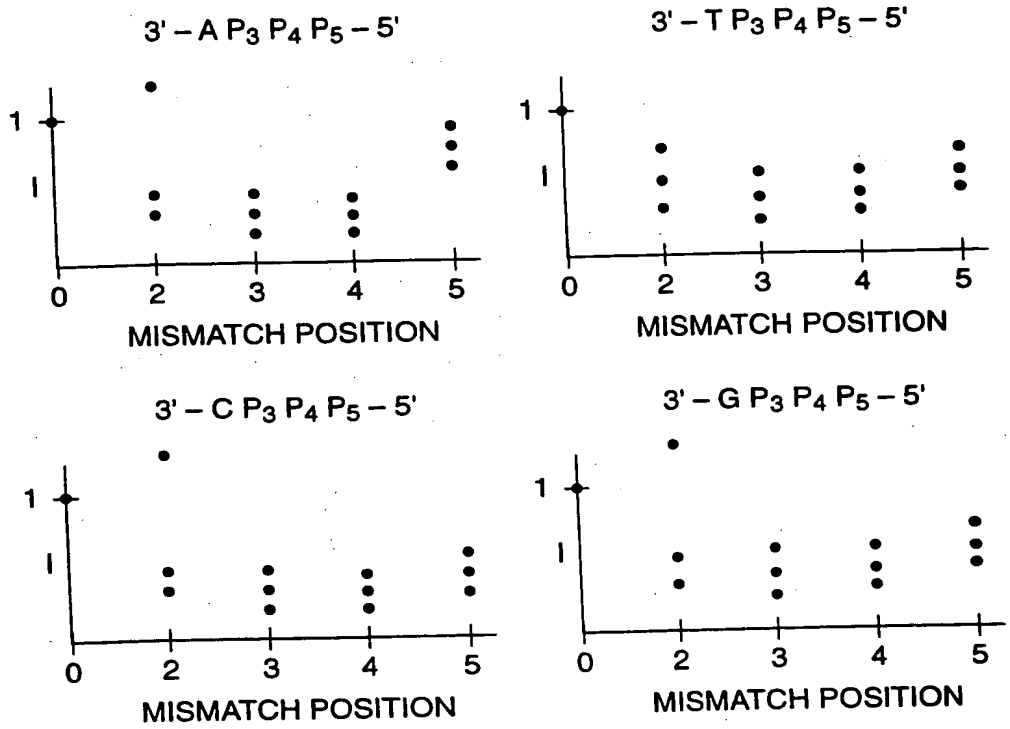


FIG. 12d

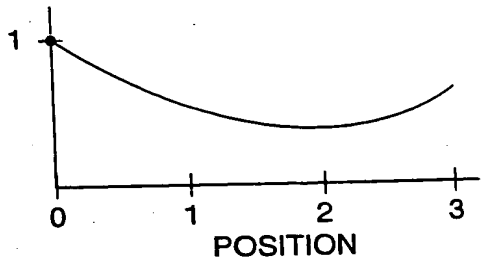


FIG. 15a

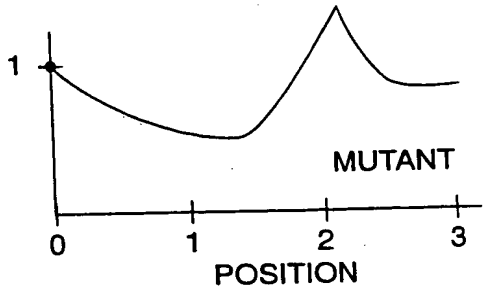


FIG. 15b

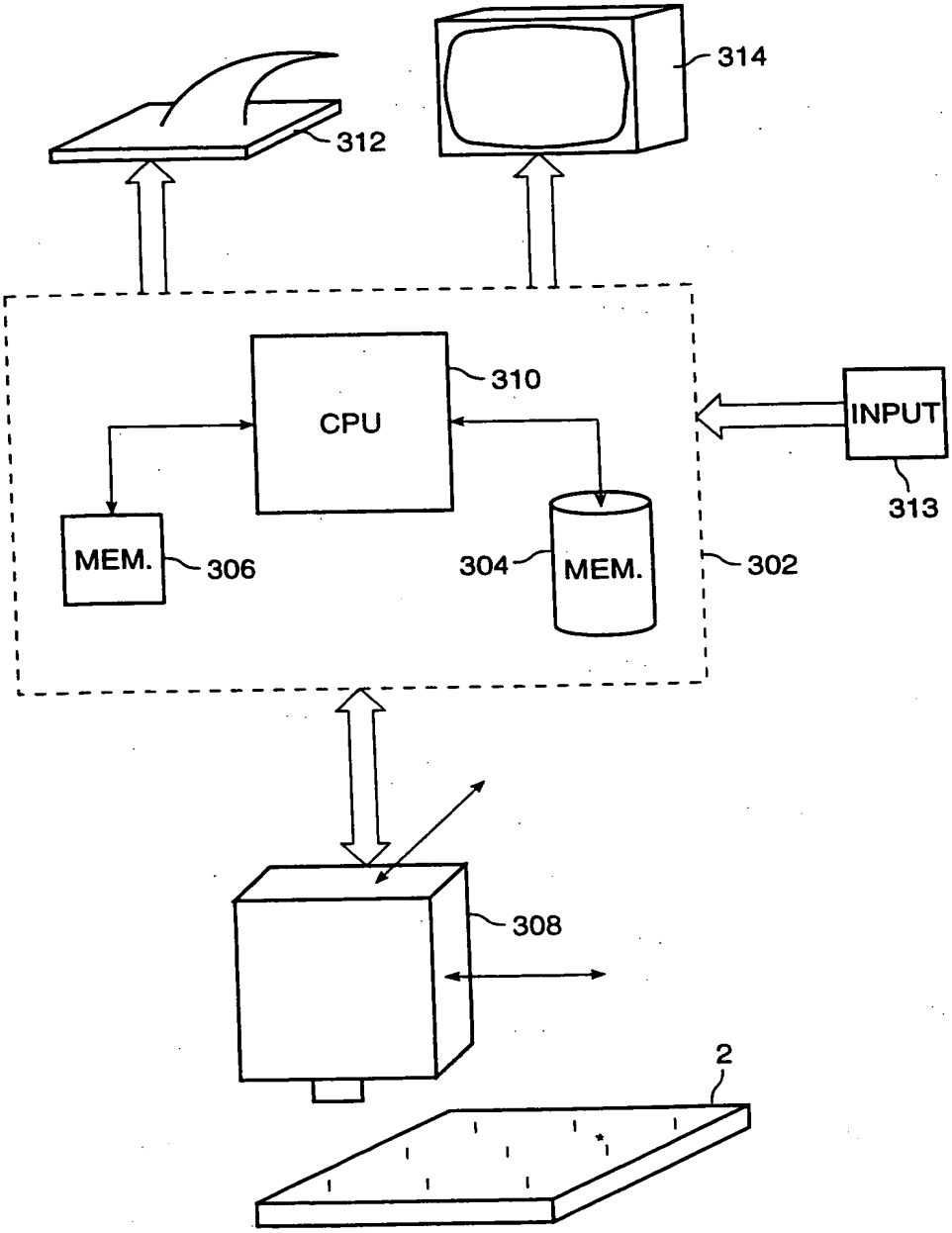


FIG. 13

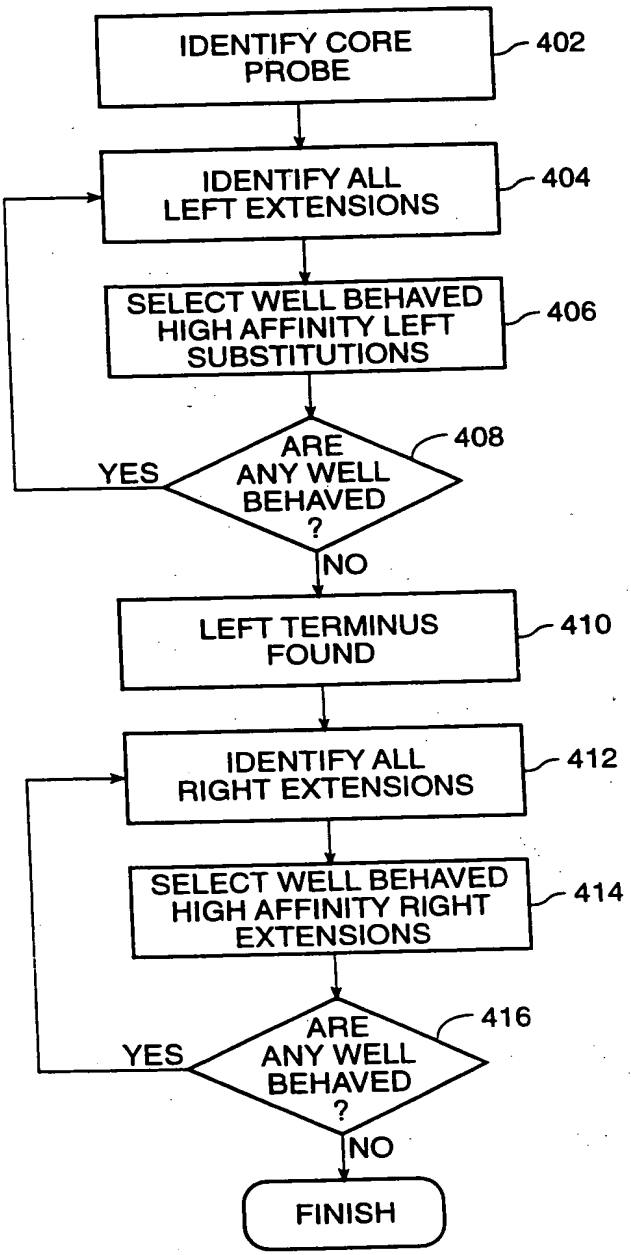

IDENTIFY CORE PROBE
402
IDENTIFY ALL LEFT EXTENSIONS
404
SELECT WELL BEHAVED HIGH AFFINITY LEFT SUBSTITUTIONS
406
ARE ANY WELL BEHAVED ?
408
YES
NO
LEFT TERMINUS FOUND
410
IDENTIFY ALL RIGHT EXTENSIONS
412
SELECT WELL BEHAVED HIGH AFFINITY RIGHT EXTENSIONS
414
ARE ANY WELL BEHAVED ?
416
YES
NO
FINISH

FIG. 14

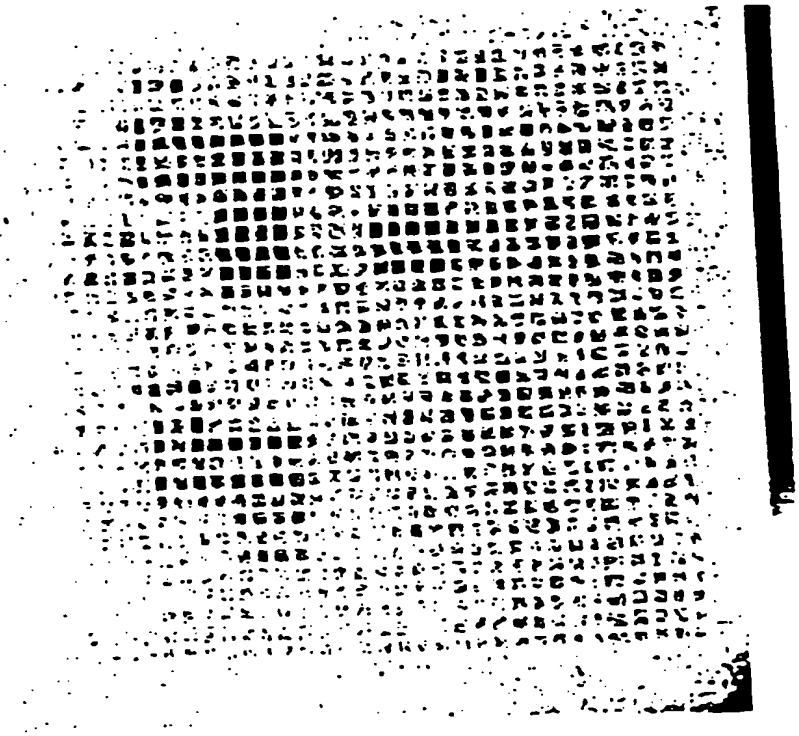


FIG. 16

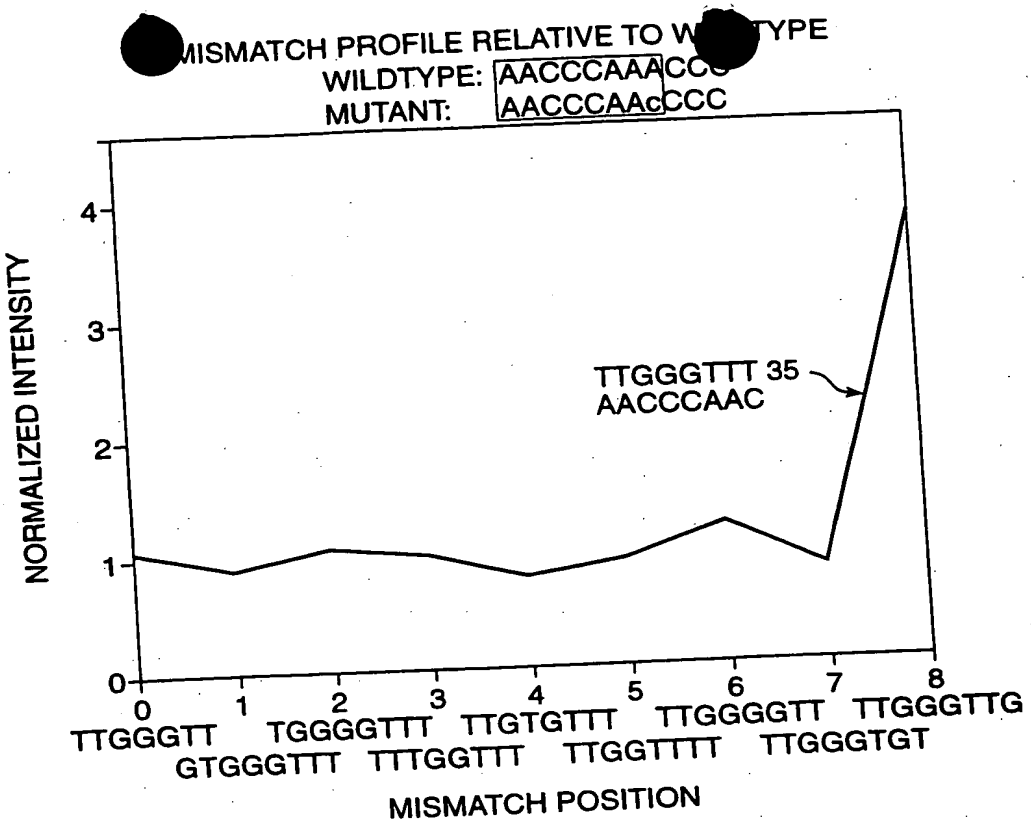


FIG. 17a

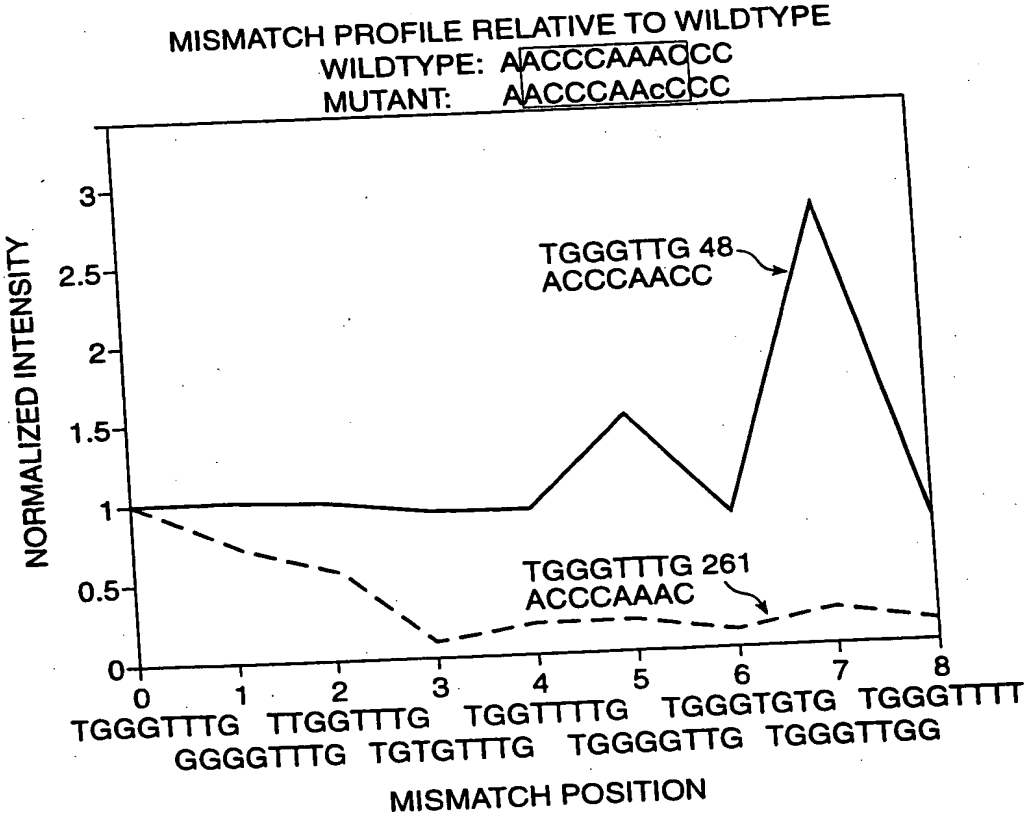


FIG. 17b

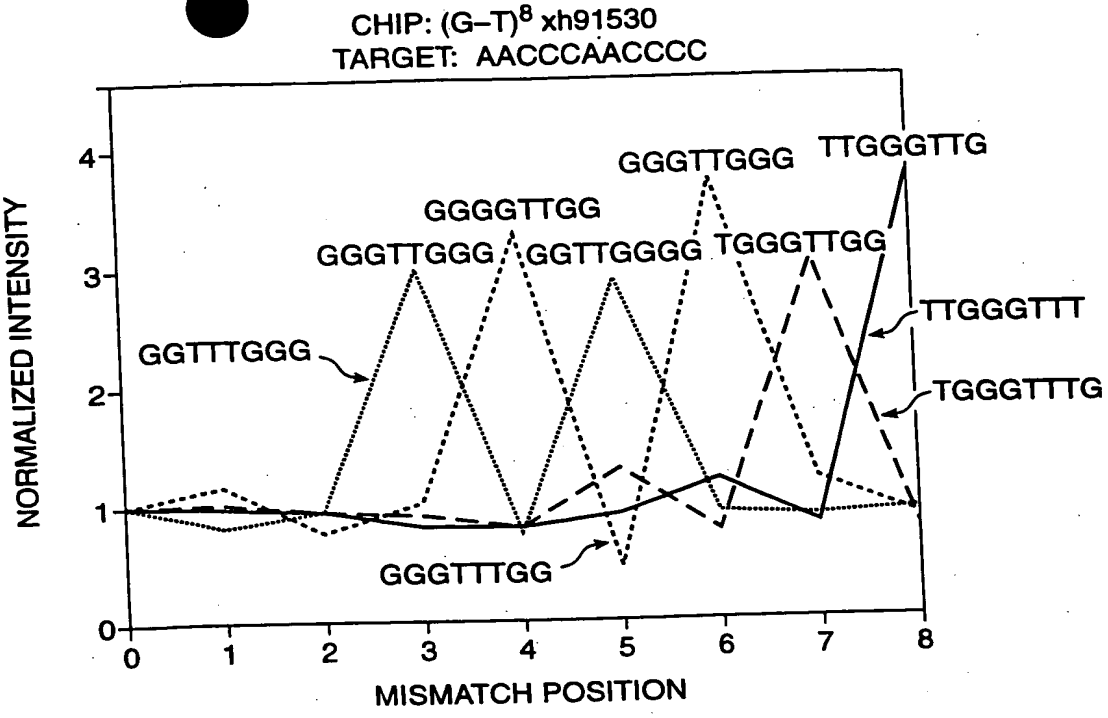


FIG. 17c

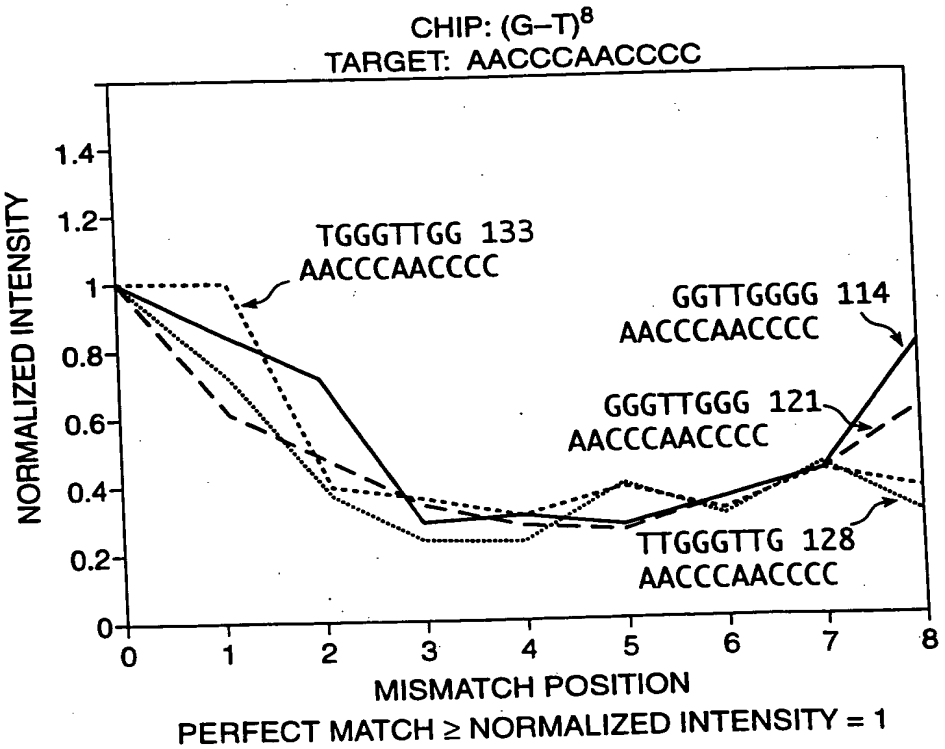


FIG. 17d